

| non-sense primer | 3'- | ATACTCTGACTCTGGGGGAGACA | -5 |
|-------------------|-------|--|----|
| sense primer | 5'- | TGAGACC <u>C</u> CCTCTGTTATCCCAG | -3 |
| Bet v 1 non-sense | 3 ' - | ${\tt TTAATACTCTGACTCTGG\underline{T}GGAGACAATAGGGTCGTCGAGC}$ | -5 |
| Bet v 1 sense | 5'- | ${\tt AATTATGAGACTGAGACC} \underline{{\tt ACCTCTGTTATCCCAGCAGCTCG}}$ | -3 |

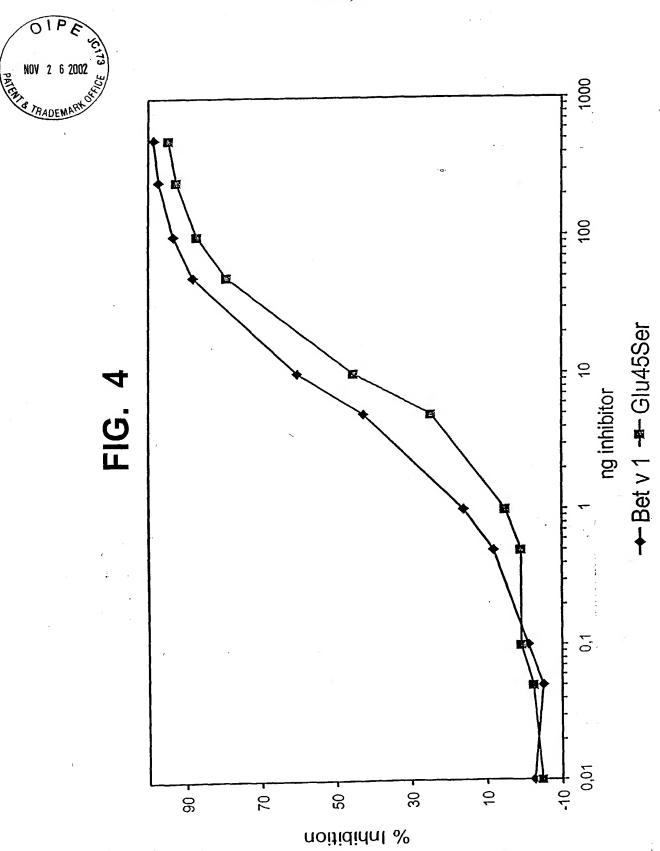


| all | sense | 1: 183Bv, 15-mer 5'-GTTGCCAACGATCAG |
|-----|-----------|---|
| 1 | sense | 2: 184Bv, 23-mer 5'-TGAGACCCCCTCTGTTATCCCAG |
| 1 | non-sense | 3: 185Bv, 23-mer 5'-ACAGAGGGGGTCTCAGTCTCATA |
| 2 | sense | 4:186Bv, 31-mer 5'-GATACCCTCTTTCCACAGGTTGCACCCCAAG |
| 2 | non-sense | 5: 187Bv, 31-mer 5'-ACCTGTGGAAAGAGGGTATCGCCATCAAGGA |
| 3 | sense | 6: 188Bv, 23-mer 5'-AACATTTCAGGAAATGGAGGCC |
| 3 | non-sense | 7: 189Bv, 23-mer 5'-TTTCCTGAAATGTTTTCAACACT |
| 4 | sense | 8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTTCCCGAA |
| 4 | non-sense | 9: 191Bv, 23-mer 5'-AGCTGATGTTCTTAATGGTTCCA |
| S | sense | 10: 192Bv, 23-mer 5'-GGACCATGCAAACTTCAAATACA |
| 5 | non-sense | 11: 193Bv, 23-mer 5'-AGTTTGCATGGTCCACCTCATCA |
| 6 | sense | 12: 194Bv, 23-mer 5'-TTTCCCTCAGGCCTCCCTTTCAA |
| 6 | non-sense | 13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAAGCTGATCTT |
| 7 | sense | 14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGGCCTGGAAC |
| 7 | non-sense | 15: 197Bv, 24-mer 5'-CCCTCCAGATCCTTCAATGTTTTC |
| 8 | sense | 16: 198Bv, 24-mer 5'-GGCAACTGGTGATGGAGGATCCAT |
| 8 | non-sense | 17: 199Bv, 24-mer 5'-CCATCACCAGTTGCCACTATCTTT |
| n11 | non-sense | 18: 200By 15-mer 5'-CATGCCATCCGTAAG |

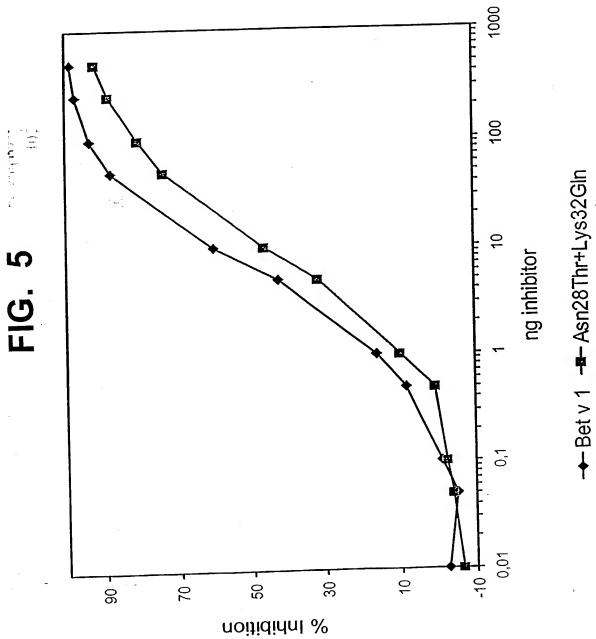


| | | | | | | | | 1 | (A-C | 2) | | | | | | | | | | |
|-------|---------------------------------------|---|--|--|--|---|---|---|--|---|---|--|---|--|--|---|---|---|---|---|
| IGI | GTT | TAA | TTA | rga | GAC | TGA | GAC | CAC | CTC | TGT | TAT | ccc | CAGC | AGC | TCG | ACT | GT | rc. | AAG | 60 |
| v | F | N | Y | E | r : | E | r | Г Т~ | PS | ; · | 7 1 | . I | A | A | R | L | E | ? | ĸ | 20 |
| | | | | | | | | | | | | | | | | | | | | |
| | | | 9 (A- | -G) | | 2 | (A- | C) | 2 (A | C) | | | | | | | | | | |
| TT | raty | CCT | TG <u>A</u> T | GG | CGA | TAA | CCI | CTT | TCC | AAA | .GGT | TGC | ACCC | CA | AGC | CAT | TAG | C | AGT | 120 |
| F | 1 | L | D-G | G | D | N-' | ГL | F | P | к- | Q V | А | . 1 2- | Q | A | I | s | ; | s | 40 |
| | | | | | | | | | | | | | | | | | | | | |
| | 3 ((| - A | TC) | | 7 (A. | A-19 | C) | | | | | | (G-C | :) | | 6 | (GA | - 1 | rc) | |
| YGA A | - | | - | | - | | • | GCC | rgg | AAC | CAT | | | | | | | | - | 180 |
| | | | | | | | | | | | | | | | | | | | | 60 |
| £ | 14 | 1 | E-3 | G | 14-1 | . . | G | F | G | • | | | K-K | • | 3 | E | • | | 5 | 80 |
| | | | | | | | | | | | | | | _ | . / | m/ | | | | |
| | | | | | | | | | | | | | | | | | | | | |
| CTC | CCI | TTC | CAAG | TAC | CTC | GAAC | GA | CAG | AGT | rga: | rga(| GTV | GGAC | CAC | <u>'A</u> CA | AAC | TT | CA | AA | 240 |
| L | P | F | K | Y | V | K | D | R | V | D | E | V | D | H | T-A | N | F | | K | 80 |
| | | | | | | | | | | | | | • | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
| AAT | TAC | AGC | GTG | ATC | GAG | GGC | GG1 | rccc | TA: | \GG(| GAC | AC | ATTG | GAG | AAG | ATC | TCC | CA | AC | .300 |
| N | Y | s | v | I | E | G | G | P | I | G | D | T | £ | E | K | I | s | 1 | N | 100 |
| | | | | | | | | | | | | | | | | | | | | |
| GAG | -CA | C) | | 8 | (CC | C-T | GG) | | | | | | | | | | | | | |
| ATA | AAG. | ATA | GTGC | SCA | AC <u>C</u> | <u>CC</u> T | GAI | GGA | GGA | TCC | ATC | TTC | AAG | ATC | AGC. | AAC | AAC | T | AC | 360 |
| r | ĸ | 1 | v | A | Т | P-G | D | , G | G | s | I. | L | ĸ | r | s | N | к | • | Y | 120 |
| | | | | | | | | | | | | | | | | | | | | |
| ACC/ | LAA | GGT | GACC | CAT | GAG | GTG | AAG | GCA | GAG | CAG | GTT | AAC | GCA, | AGT. | AAA | GAA | ATC | GG | ЗC | 420 |
| т | ĸ | G | D | н | E | v | κ. | A | Е | Q | v | ĸ | A | s | ĸ | E | м | (| 3 . | 140 |
| | | | | | | | | | | | | | | | | | | | | |
| \CA(| TT; | rtg | AGGG | CC | GTT | GAG. | AGC | TAC | СТС | TTG | GCA | CAC | TCCC | TAG | GCC | TAC. | AAC | T | A .A | 480 |
| т | , | | b | | ., | E | c | v | | | Λ. | u | e | D | n | v | N T | ۰. | - 00 | 150 |
| | V F F GAA E CTC L AAAT N AAAT I AACCA | V F TITATO F I 3(C GAAAAC E N CTCCCI L P AATTAC ATAAAG I K ACCAAAC T K | V F N CTTTATCCT F I L 3 (GA GAAAACAT E N I CTCCCTTTV L P F AATTACAGC N Y S GAG-CAC) ATAAAGATA I K I ACCAAAGGT T K G | 9 (A- TITATCCTTGAT F I L D-G 3 (GA-TC) GAAAACATTGAA E N I E-S CTCCCTTTCAAG L P F K AATTACAGCGTGA N Y S V GAG-CAC) ATAAAGATAGTCC I K I V ACCAAAGGTGACC T K G D | 9 (A-G) TTTATCCTTGATGG F I L D-G G 3 (GA-TC) GAAAACATTGAAGG E N I E-S G CTCCCTTTCAAGTAC L P F K Y AATTACAGCGTGATC N Y S V I GAG-CAC) E ATAAAGATAGTGGCA I K I V A ACCAAAGGTGACCAT T K G D H | 9 (A-G) TTTATCCTTGATGGCGA F I L D-G G D 3 (GA-TC) 7 (A GAAAACATTGAAGGAAA E N I E-S G N-S CTCCCTTTCAAGTACGTA L P F K Y V AATTACAGCGTGATCGAC N Y S V I E GAG-CAC) 8 (CC ATAAAGATAGTGGCAACC I K I V A T ACCAAAGGTGACCATGAG T K G D H E | 9 (A-G) 2 CTTTATCCTTGATGGCGATAA F I L D-G G D N- 3 (GA-TC) 7 (AA-TC GAAAACATTGAAGGAAATGG E N I E-S G N-S G CTCCCTTTCAAGTACGTGAAC L P F K Y V K AATTACAGCGTGATCGAGGGC N Y S V I E G GAG-CAC) 8 (CCC-TC ATAAAGATAGTGGCAACCCCT I K I V A T P-G ACCAAAGGTGACCATGAGGTG T K G D H E V | 9 (A-G) 2 (A-CTTTATCCTTGATGGCGATAACCT F I L D-G G D N-T L 3 (GA-TC) 7 (AA-TC) GAAAACATTGAAGGAAATGGAGG E N I E-S G N-S G G CTCCCTTTCAAGTACGTGAAGGAA L P F K Y V K D AATTACAGCGTGATCGAGGGCGGT N Y S V I E G G GAG-CAC) 8 (CCC-TGG) ATAAAGATAGTGGCAACCCCTGAT I K I V A T P-G D ACCAAAGGTGACCATGAGGTGAAG T K G D H E V K | POTENTIANTENTAGAGACTGAGACCAC V F N Y E T E T T- 9 (A-G) 2 (A-C) TITTATCCTTGATGGCGATAACCTCTT F I L D-G G D N-T L F 3 (GA-TC) 7 (AA-TC) GAAAACATTGAAGGAAATGGAGGGCC E N I E-S G N-S G G P CTCCCTTTCAAGTACGTGAAGGACAGA L P F K Y V K D R AATTACAGCGTGATCGAGGGCGGTCCC N Y S V I E G G P GAG-CAC) 8 (CCC-TGG) ATAAAGATAGTGGCAACCCCTGATGGA I K I V A T P-G D G ACCAAAGGTGACCATGAGGTGAAGGCAACCACAAAGGTGACCATGAGGTGAAGGCAACCACAAAGGTGACCATGAGGTGAAGGCAACACCACAAAGGTGACCATGAGGTGAAGGCAACACCACTTTTGAGGGCCCTTGAGGAGCTACACACCTTTTGAGGGCCCCTTGAGGAGCTACACACCTTTTGAGGGCCCCTTGAGGAGCTACACACCTTTTTGAGGGCCCCTTGAGGAGCTACACACCTTTTTGAGGGCCCCTTGAGAGGCTACACACCTTTTTGAGGGCCCCTTGAGAGGCTACACACCTTTTTGAGGGCCCCTTGAGAGCTACACACCTTTTTGAGGGCCCCTTGAGAGCTACACACTTTTTGAGGGCCCCTTGAGAGCTACACACTTTTTGAGGGCCCCTTGAGAGCTACACACTTTTTGAGGGCCCCTTGAGAGCTACACACTTTTTGAGGGCCCCTTGAGAGCTACACACTTTTTGAGGGCCCCTTGAGAGCTACACACTTTTTGAGGGCCCCTTGAGAGCTACACACTTTTTGAGGGCCCCTTGAGAGCTACACACTTTTTGAGGGCCCCTTGAGGAGCTACACACAC | PAGE TO THE TOTAL POST OF THE | 9 (A-G) 2 (A-C) 2 (A-C) TITATCCTTGATGGCGATAACCTCTTTCCAAA F I L D-G G D N-T L F P K- 3 (GA-TC) 7 (AA-TC) GAAAACATTGAAGGAAATGGAGGGCCTGGAAC E N I E-S G N-S G G P G T CTCCCTTTCAAGTACGTGAAGGACAGAGTTGA: L P F K Y V K D R V D AATTACAGCGTGATCGAGGGCGGCCCCATAGGC N Y S V I E G G P I G GAG-CAC) 8 (CCC-TGG) ATAAAGATAGTGGCAACCCCTGATGGAGGATCC I K I V A T P-G D G G S ACCAAAGGTGACCATGAGGTGAAGGCAGAGCAG T K G D H E V K A E Q | PARTITICATE AND A CONTROL OF THE AND A COMMANDE TO THE ACCAMAGGT GRAND CONTROL OF THE ACCAMAGGT GRAND GRAND CONTROL OF THE ACCAMAGGT GRAND GRA | PATTACAGCATCAGACCAGCACCACCACCACCACCACCACCACCACCACCA | PATTACAGCGTGATCGAGACCACCTCTGTTATCCCAGC O F N Y E T E T T-P S V I P A 9 (A-G) 2 (A-C) 2 (A-C) TITTATCCTTGATGGCGATAACCTCTTTCCAAAGGTTGCACCC F I L D-G G D N-T L F P K-Q V A P 3 (GA-TC) 7 (AA-TC) 4 (G-C) GAAAACATTGAAGGAAATGGAGGGCCTGGAACCATTAAGAAG E N I E-S G N-S G G P G T I K K-N CTCCCTTTCAAGTACGTGAAGGACAGAGTTGATGAGGTGAC L P F K Y V K D R V D E V D AATTACAGCGTGATCGAGGGCGGTCCCATAGGCGACCATTGAAGA N Y S V I E G G P I G D T L GAG-CAC) 8 (CCC-TGG) ATAAAGATAGTGGCAACCCCTGATGGAGGATCCATCTTGAAGI I K I V A T P-G D G G S I L K ACCAAAGGTGACCATGAGGTGAAGGCAGAGCAGGTTAAGGCAI T K G D H E V K A E Q V K A | PARTITION OF THE TOTOPS VIPA A 9 (A-G) 2 (A-C) 2 (A-C) TITTATCCTTGATGGCGATAACCTCTTTCCAAAGGTTGCACCCCA FILD-GGDN-TLFPK-QVAPQ 3 (GA-TC) 7 (AA-TC) 4 (G-C) GAAAACATTGAAGGAAATGGAGGGCCTGGAACCATTAAGAAGATGATGAGGTGAACCATTAAGAAGATGATGAGGTGAACCATTAAGAAGATGATGAAGGAAATGGAAGGACAGAGTTGATGAGGTGAACCATTAAGAAGATAAGAAGATGAAGAAGATGAAGAAGATGAAGAA | PORTOTITIANTINTEGRACTORIGACCACCTCTGTTATCCCAGCAGCTCG V F N Y E T E T T-P S V I P A A R 9 (A-G) | POTESTITIANTINTEGRACTORIGACCACCTCTGTTATCCCAGCAGCTCGACT V F N Y E T E T T-P S V I P A A R L 9 (A-G) 2 (A-C) 2 (A-C) TITATCCTTGATGGCGATAACCTCTTTCCAAAGGTTGCACCCCAAGCCAT F I L D-G G D N-T L F P K-Q V A P Q A I 3 (GA-TC) 7 (AA-TC) 4 (G-C) 6 GAAAACATTGAAGGAAATGGAGGGCCTGGAACCATTAAGAAGATCAGCTT E N I E-S G N-S G G P G T I K K-N I S F 5 (CA-TC CTCCCTTTCAAGTACGTGAAGGACAGAGTTGATGAGGTGACCACACAAAC L P F K Y V K D R V D E V D H T-A N AATTACAGCGTGATCGAGGGCGGGTCCCATAGGCGACACATTGGAGAAGAT N Y S V I E G G P I G D T L E K I GAG-CAC) 8 (CCC-TGG) ATAAAGATAGTGGCAACCCCTGATGGAGGATCCATCTTGAAGATCAGCAAC I K I V A T P-G D G G S I L K I S N ACCAAAGGTGACCATGAGGTGAAGGCAGGAGCAGGTTAAGGCAAGTAAAGAA T K G D H E V K A E Q V K A S K E | POTENTIANT ATTATES GACTES AGAC CACCTCT GTTATCCCAGCAGCT GACTET. V F N Y E T E T T-PS V I P A A R L I 9 (A-G) 2 (A-C) 2 (A-C) TITTATCCTTGATGGCGATAACCTCTTTCCAAAGGTTGCACCCCAAGCCATTAG F I L D-G G D N-T L F P K-Q V A P Q A I S 3 (GA-TC) 7 (AA-TC) 4 (G-C) 6 (GA GAAAAACATTGAAGGAAATGGAGGGCCCTGGAACCATTAAGAAGATCAGCTTTCC E N I E-S G N-S G G P G T I K K-N I S F P 5 (CA-TG) CTCCCTTTCAAGTACGTGAAGGACAGAGTTGATGAGGTGGACCACAAAACTT L P F K Y V K D R V D E V D H T-A N F AATTACAGCGTGATCGAGGGCGGTCCCATAGGCGACACATTGGAGAAGATCTCC N Y S V I E G G P I G D T L E K I S GAG-CAC) 8 (CCC-TGG) ATAAAGATAGTGGCAACCCCCTGATGGAGGATCCATCTTGAAGATCAGCAACAAC I K I V A T P-G D G G S I L K I S N K ACCAAAAGGTGACCATGAGGTGAAGGCAGGGTTAAGGCAAGTAAAGAAATC T K G D H E V K A E Q V K A S K E M ACCACTTTTGAGGGCCGTTGAGAGCTACCTCTTGGCACACTCCGATGCCTACAAC | PATTACATTA ATTATA AGA CTAGA CCACCTCT ATTATC CCAGCA GCTCACACCTCT CCAGCA GCTCACACCTCT CCAGCA GCTCACACCTCT CCAGCA GCTCACACCTCT CCAGCA GCCCCAAGCCATTAGCAGCACTCT CCAGCACTTAGCAGCACTCT CCAGCACTTAGCAGCACTCT CCAGCACTTAGCAGCACTCT CCAGCACTTAGCAGCACCTCT CCAGCACTTAGCAGCACCTCT CCAGCACTTAGCAGCACCACTCCAGCACACCTCCAGCACCTCCAGCACCTCCAGCACCACTAGCAGCACCACTCCAGCACACCTCCAGCACCACCACCACCACACCACCACACCACACACCACACCACCACA | TOTATION TO THE TOTAL PROPERTY OF THE TOTAL |

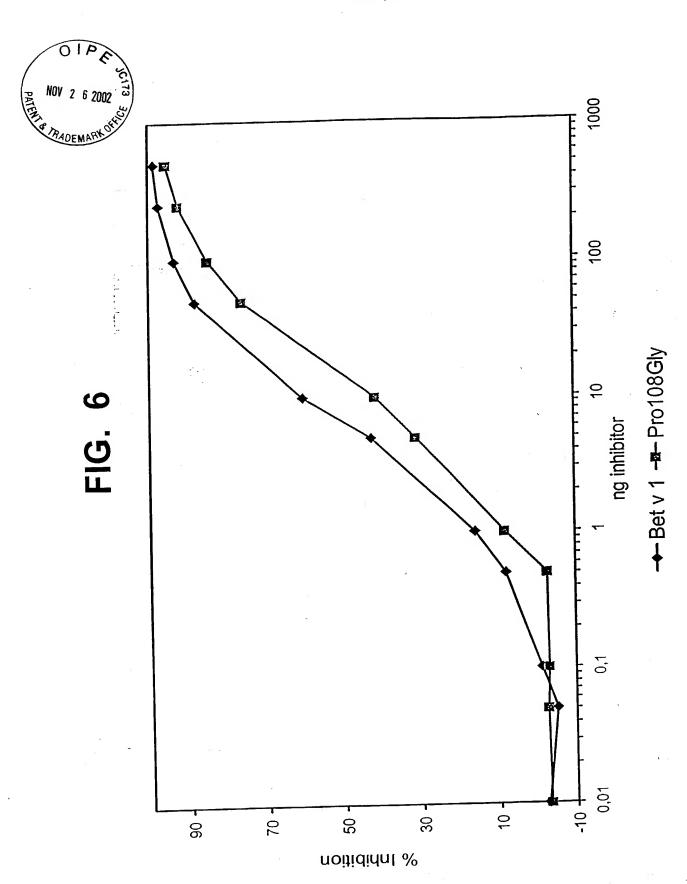


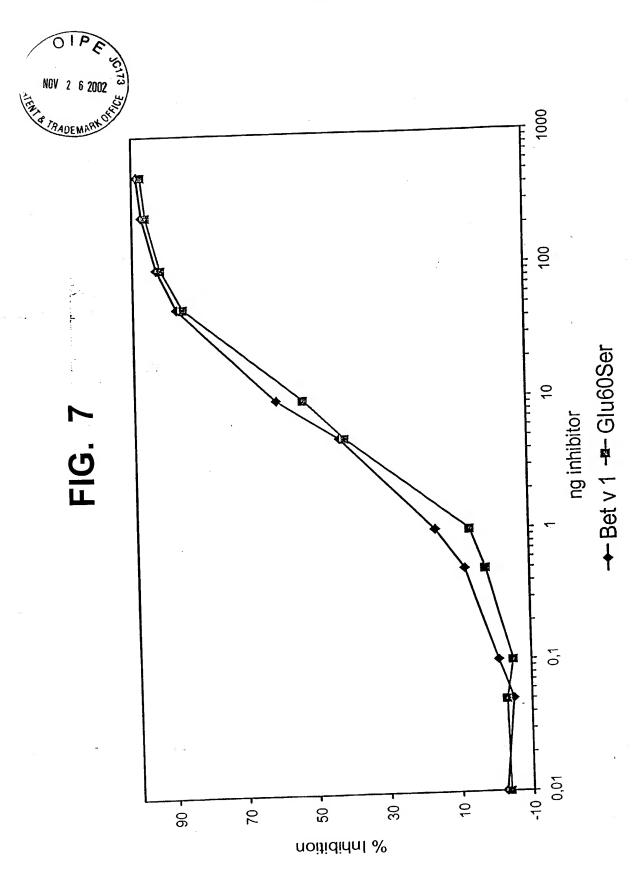


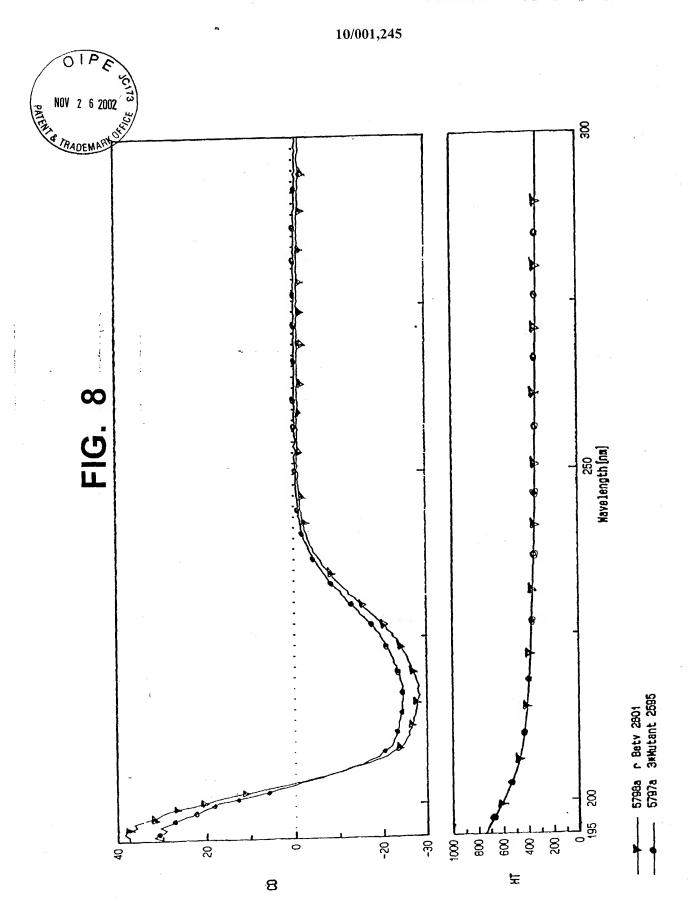




10/001,245







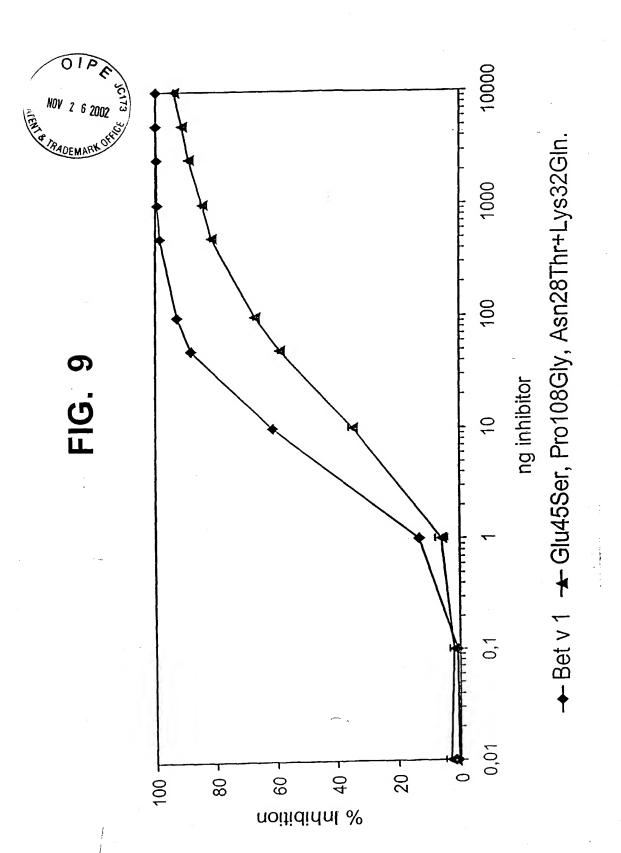




FIG. 10 A

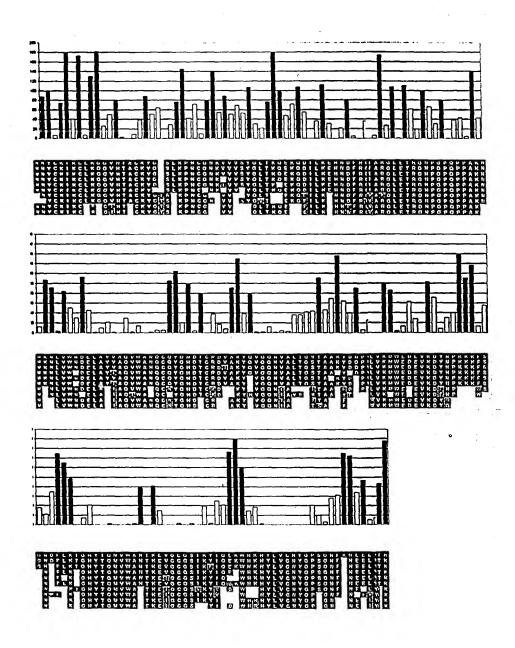




FIG. 10 B

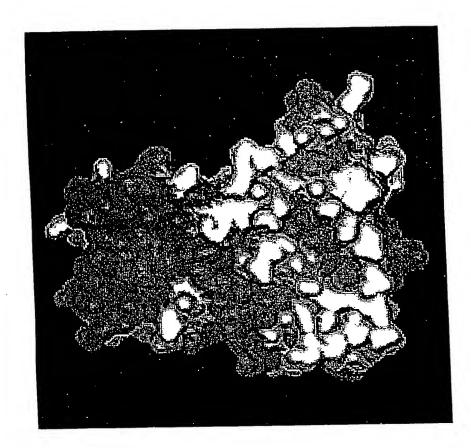




FIG. 11 A

Ves v 5 mutant 1 (K72A)

| Ves v 5 sense | 5 - | ACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGA | -31 |
|-------------------|-------|---|-----|
| Ves v 5 non-sense | 3 ~ - | ${\tt TGGTGTCGGAGGTCGCTTCTTATACTTTTTAAACCATACCT}$ | -51 |
| sense primer | 5^~ | CCAGCG <u>GCT</u> AATATGAAAAAT | -31 |
| non-sense primer | 3'- | GTCGGAGGTCGC <u>CGA</u> TTATAC | -51 |

FIG. 11 B

Ves v 5 mutant 2 (Y96A)

| Ves v 5 sense | 5^- | ${\tt GGCTAATCAATGTCAATATGGTCACGATACTTGCAGGGATG}$ | -3 ^ |
|-------------------|-------|---|------|
| Ves v 5 non-sense | 3′- | ${\tt CCGATTAGTTACAGTTATACCAGTGCTATGAACGTCCCTAC}$ | -5´ |
| sense primer | 5^- | TGTCAA <u>GC</u> TGGTCACGATACT | -3~ |
| non-sense primer | 3 ~ - | TTAGTTACAGTT <u>CG</u> ACCAGTG | -5~ |

FIG. 12

all sense 1: XhoI start, 38-mer:

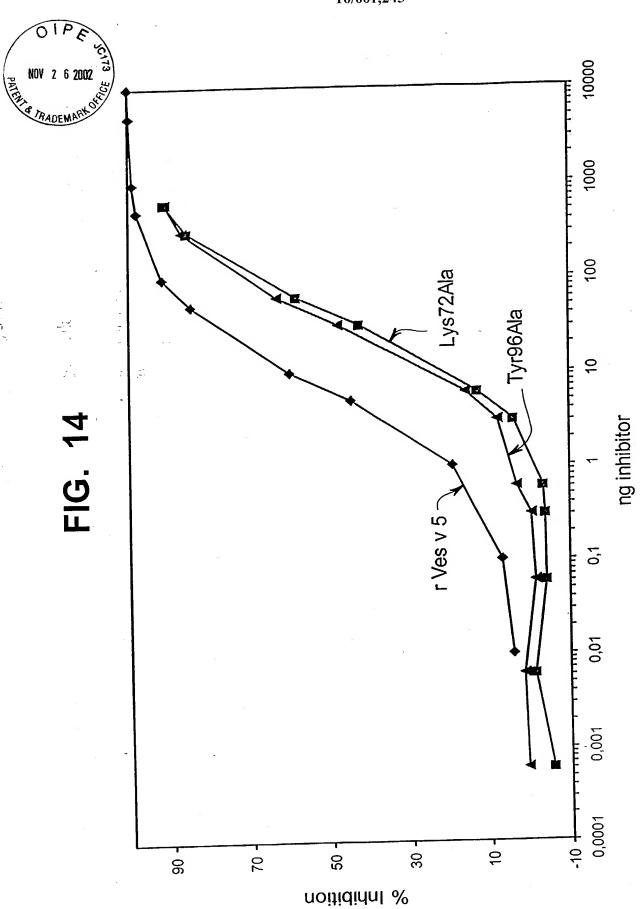
EcoRI 5 - CCGCTCGAGAAAGAAACAATTATTGTAAAATAAATG L E K R N N Y C K I K Kex2 cleavage site amino terminus of Ves v 5

| <pre>1 sense 1 non-sense</pre> | 1: K72As 21-mer 2: K72Aa 21-mer | 5´-CCAGCGGCTAATATGAAAAAT 5´-CATATTAGCCGCTGGAGGCTG |
|--------------------------------|------------------------------------|--|
| 2 sense 2 non-sense | 3: Y96As 21-mer 4: Y96Aa 21-mer | 5´-TGTCAAGCTGGTCACGATACT 5´-GTGACCAGCTTGACATTGATT |
| all non-sense | 7: CT-DPICZQA 21-me | r 5`-ATTCATCAGCTGCGAGATAGG |

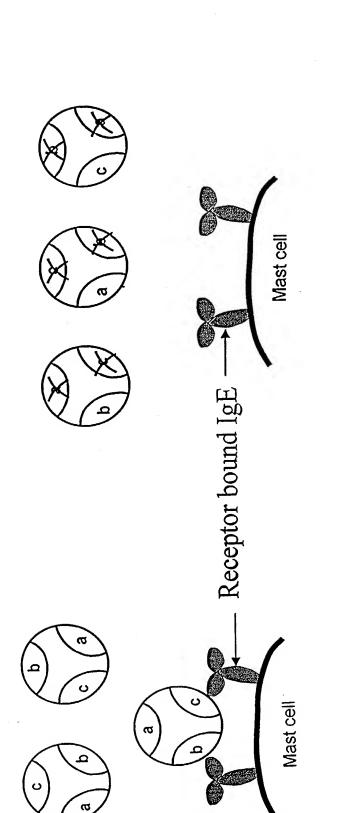


| 1 | . AA | CAA' | TTA' | TTG' | LAAT | TAP | AAA | ATG | TTT(| gaa <i>i</i> | \GG! | \GG' | rgr | CCAT | raci | GCC | CTG | CAA | ATA? | IGGA | 60 |
|-----|------|------|--------|------|---------------|------|------|------|------|--------------|------|------|------|---------|-----------------|-----|-------------|--------------------|------|------|-----|
| 1 | . N | N | Ÿ | С | K | Ĭ | K | С | L | K | G | G | V | H | Ţ | A | С | K | Y | G | 20 |
| 61 | AGT | rct" | ГААЛ | ACC | GAAT | rtgo | CGG" | raat | DAA1 | GTI | GTC | GTA | ATCO | TAT | GGI | CTA | ACC | SAAI | ACAZ | AGAG | 120 |
| | S | | | | | | | | | | | | | | | | | | | | 40 |
| | | | • | • | 2, | Ū | J | • | ••• | · | • | · | | - | | _ | - | - | × | _ | 70 |
| | | | | | | | | | | | | | | | | | | | | GAG | 180 |
| 41 | K | Q | D | 1 | L | ĸ | E | H | N | D | F | R | Q | K | Ι | A | R | G | L | Е | 60 |
| | | | | | | | | | | | | _ | K72 | | | | • | | | | |
| 181 | ACT | `AGA | GGI | raa' | CCI | GGA | CCA | CAG | CCI | CCA | .GCG | AAG | TAA | `ATG | AAA | AAT | TTG | GTA | TGG | AAC | 240 |
| 61 | T | R | G | N | P | G | P | Q | P | ·P | A | K | N | M | K | N | L | V | W | Ń | 80 |
| | | | | | | | | | | | | | | | | 2 [| Y96 | A] (| TA- | ·GC) | |
| 241 | GAC | GAG | ATT | GCI | TAT | GTC | GCC | CAA | GTG | TGG | GCT | AAT | CAA | TGT | CAA | TAT | GGT | 'CAC | GAT | ACT | 300 |
| 81 | D | E | L | A. | Y | V | A | 0 | v | W | A | N | 0 | С | 0 | Y | G | Н | D | Ť | 100 |
| | | | | | | | | _ | | | | | _ | | - | | | | | | |
| 301 | TGC | AGG | GAT | GTA | GCA. | AAA | TAT | CAG | ĠTT | GGA | CAA | AAC | GTA | GCC | TTA. | ACA | GGT | AGC | ACG | GCT | 360 |
| 101 | C | R | D | V | A | K | Y | Q | v | G | Q | N | v | Α | \mathbf{L} | T | G | S | T | A | 120 |
| | | | | | | | o. | | | | | | | | | | | | | | |
| 361 | GCT | AAA | TAC | GAT | GAT | CCA | GTT | AAA | CTA | GTT. | AAA | ATG | TGG | GAA | GAT | GAA | G TG | AAA | GAT | TAT | 420 |
| 121 | A | K | Y | D | D | P | v | K | L | V | K | M | W | Е | Ď | E | V | `K. | D | Y | 140 |
| 121 | AAT | ÇCT: | AAG. | AAA | AAG: | rtt | TCG | GGA. | AAC | GAC | rtt(| CTG. | AAA | ACC | GGC(| CAT | TAC | ACT | CAA | ATG | 480 |
| 141 | N | p | K | K | \mathbf{K}' | F | S | ď | N | D | F | L | ĸ | ${f T}$ | G | H | Ϋ́ | \mathbf{T}^{r} . | Q | M F | 160 |
| | | | | | | | | | | | | | | | | | | | | | |
| 181 | GTT | TGG | GCT | AAC | ACC | AAG | GAA | GTT | GT" | TGT | 3GA | AGT | ATA | AAA | rac <i>i</i> | ATT | CAA | GAG. | AAA' | TGG | 540 |
| | v | | | | | | | | | | | | | | | | | | | | 180 |
| | · | ., | | | - | ••• | _ | • | | | | | _ | | _ | | • | | | | |
| 41 | CAC | AAA | ייתמיי | TAC | אריתיי | TATE | тст | ייים | ידעי | GA(| CC | AGC | GA) | AAC | ידידיו <i>ן</i> | AAG | ידב | GAG | JAAE | CTT | 600 |
| | Н | | | | | | | | | | | | | | | | | | | | 200 |
| | | | | - | _ | • | _ | | - | _ | - | - | - | | - | | | | _ | | |
| 501 | TATO | CAA | ACA | AAG' | гаа | | | | | | | | | | | | | | | | 612 |
| 0.1 | v | 0 | т | к | et. | 'n | | | | | | | | | | | | | | | 204 |









No cross-linking Cross-linking



FIG. 16 A

DNA SEQUENCE

ORIGIN

cacaaattct tctttcttcc ttactactga tcattaatct gaaaacaaaa ccaaacaaac 1 cattcaaaat gatgtacaaa attttgtgtc tttcattgtt ggtcgcagcc gttgctcgtg 61 atcaagtcga totcaaagat totgccaatc atgaaatcaa aaaagttttg gtaccaggat 121 gccatggttc agaaccatgt atcattcatc gtggtaaacc attccaattg gaagccgttt 181 tcgaagccaa ccaaaacaca aaaacggcta aaattgaaat caaagcctca atcgatggtt 241 tagaagttga tgttcccggt atcgatccaa atgcatgcca ttacatgaaa tgcccattgg 301 ttaaaggaca acaatatgat attaaatata catggaatgt tccgaaaatt gcaccaaaat 361 ctgaaaatgt tgtcgtcact gttaaagtta tgggtgatga tggtgttttg gcctgtgcta 421 ttgctactca tgctaaaatc cgcgattaaa tcaaacaaaa tttattgatt ttgtaatcac 481 aaatgattga ttttctttcc aaaaaaaaaa taaataaaat tttgggaatt c 541

FIG. 16 B

1 mmykilclsl lvaavardqv dvkdcanhei kkvlvpgchg sepciihrgk pfqleavfea 61 nqntktakie ikasidglev dvpgidpnac hymkcplvkg qqydikytwn vpkiapksen 121 vvvtvkvmgd dgvlacaiat hakird

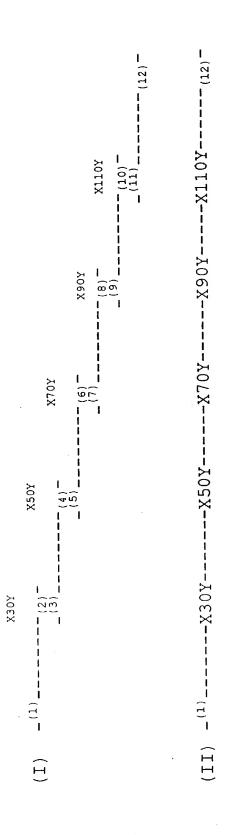






FIG. 18 A

DNA template: Bet v 1 (2589) carrying the Y5V mutation.

331pMalc (s)

189BV (a)
188BV (s)
362BV (a)
361BV (s)
364BV (a)
363BV (s)
366BV (a)
365BV (s)
332pMalc (a)

FIG. 18 B

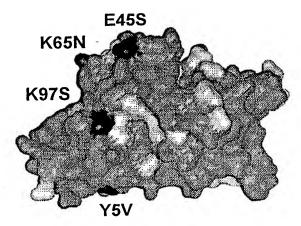
| DNA template: Bet v 1 (2571) carrying N28T | , K32Q, P108G mutations. |
|--|--------------------------|
| 331pMalc 368BVa | |
| <u>367BVs</u> 370BVa | |
| 369BVs | |

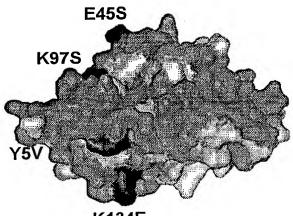
372BVa



FIG. 19 A

Bet v 1 (2628)





K134E

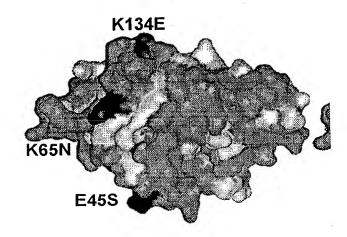
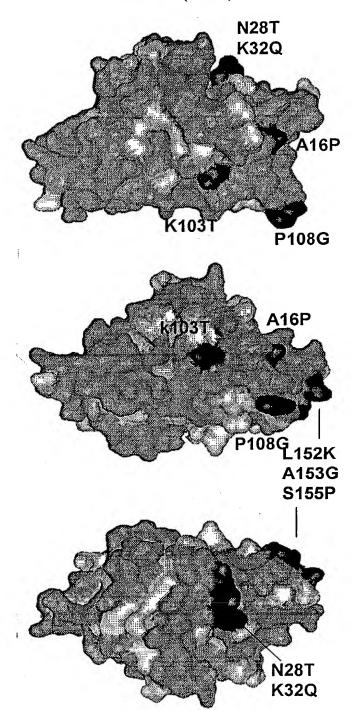
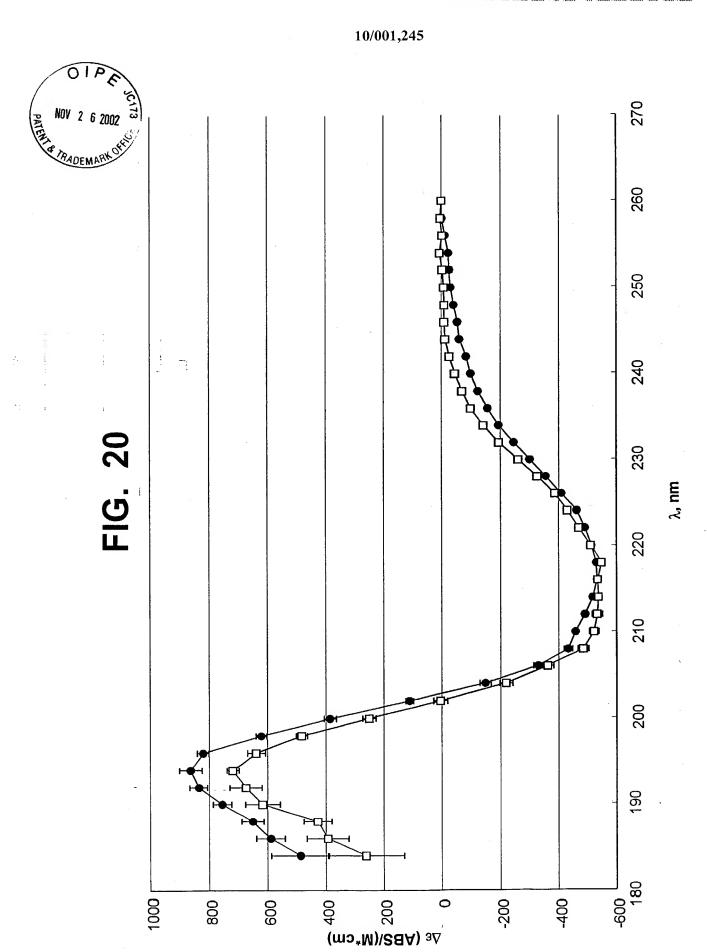


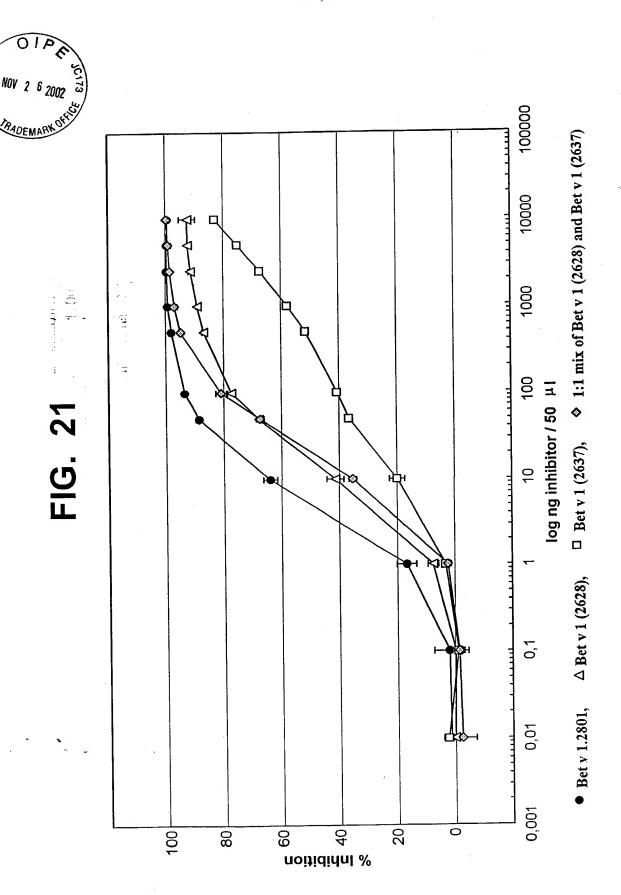


FIG. 19 B

Bet v 1 (2637)











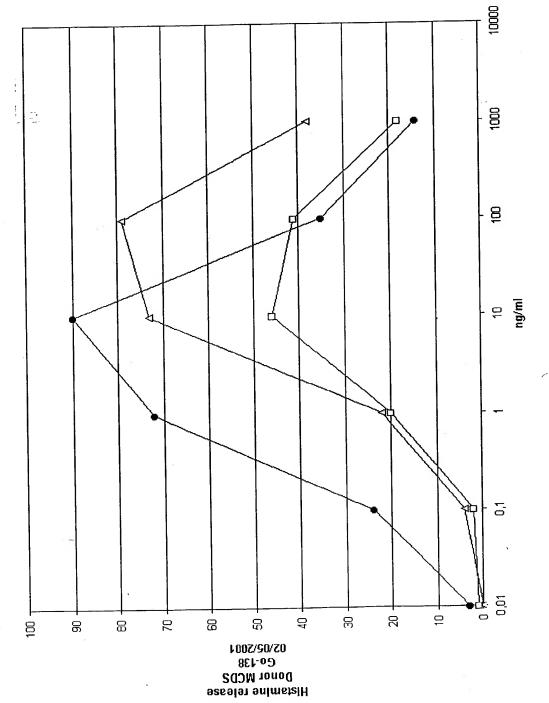
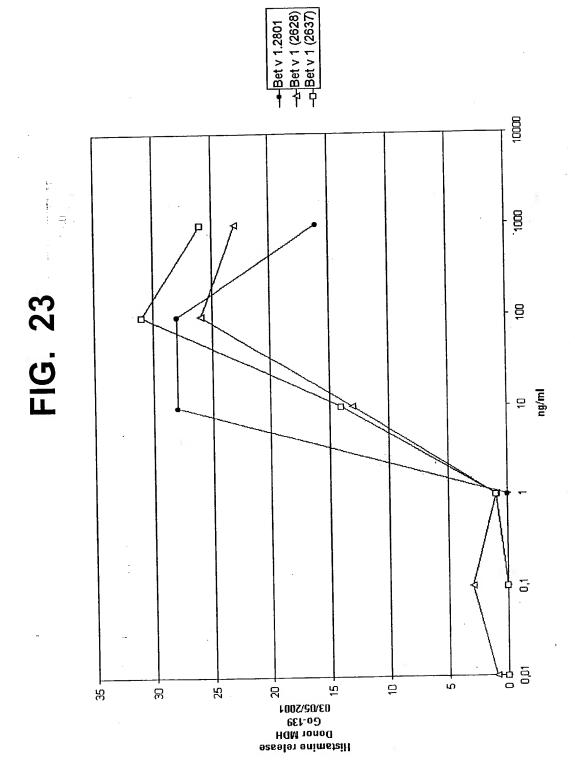
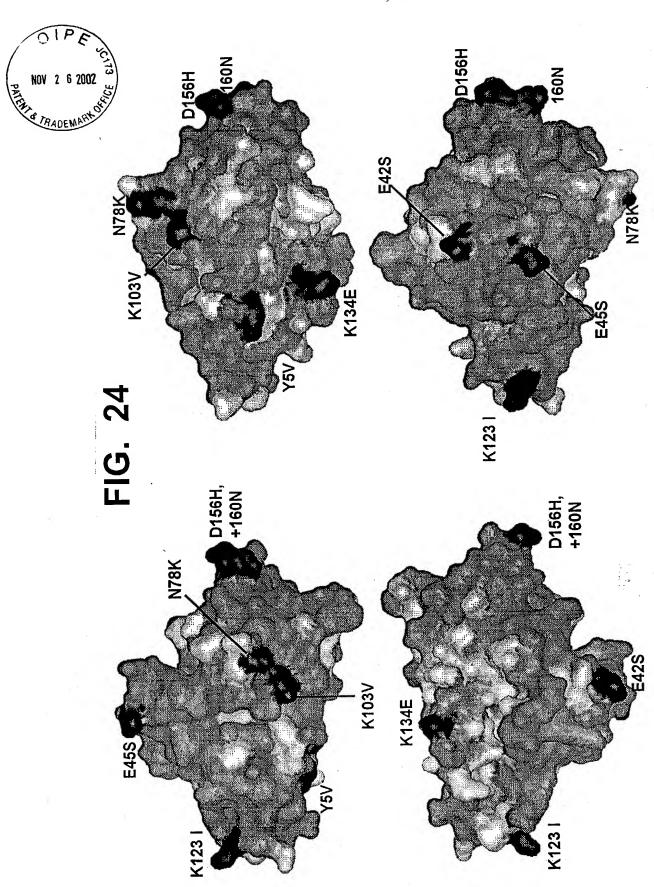
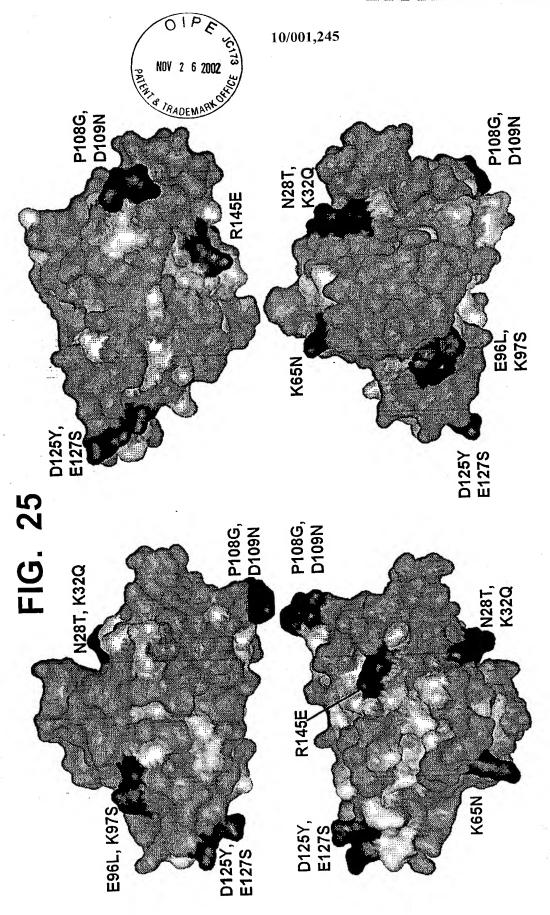
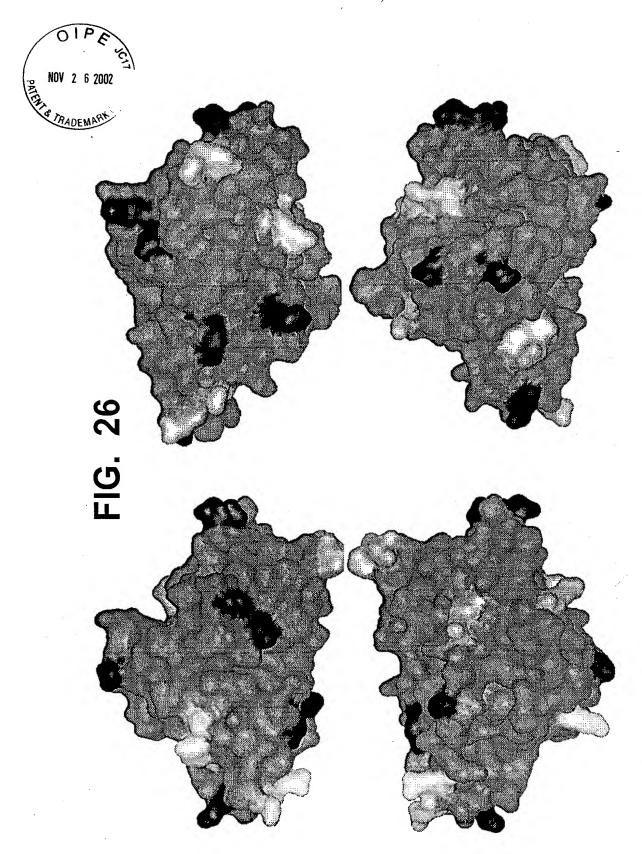


FIG. 22

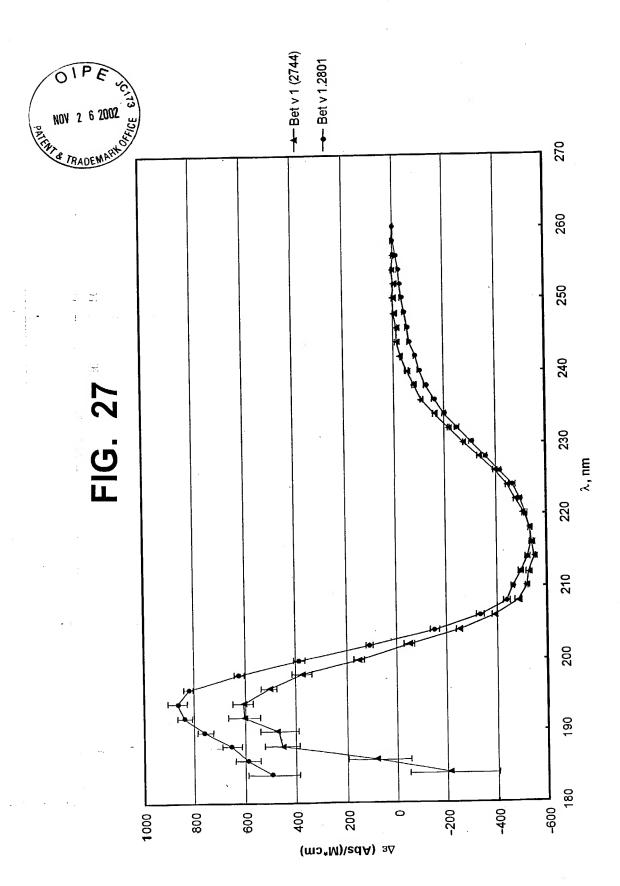


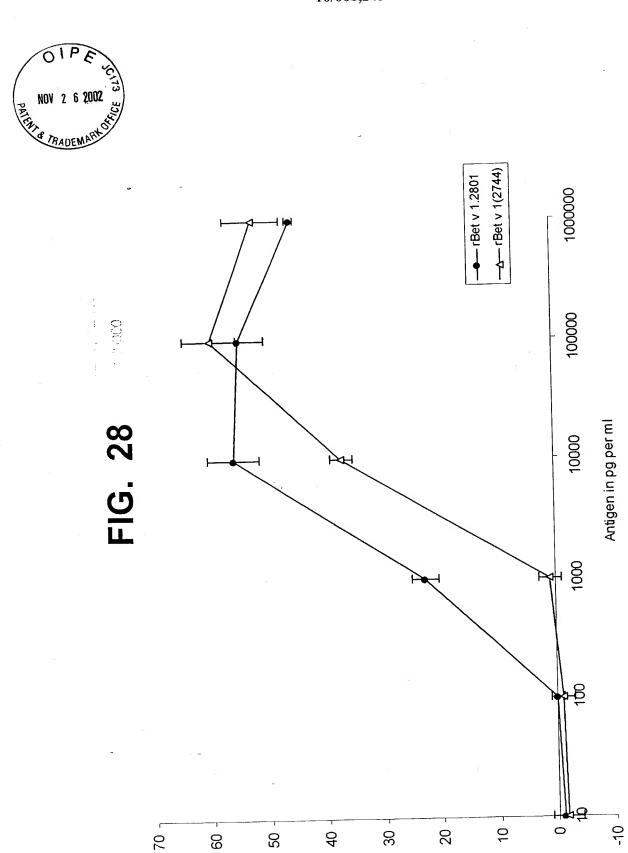




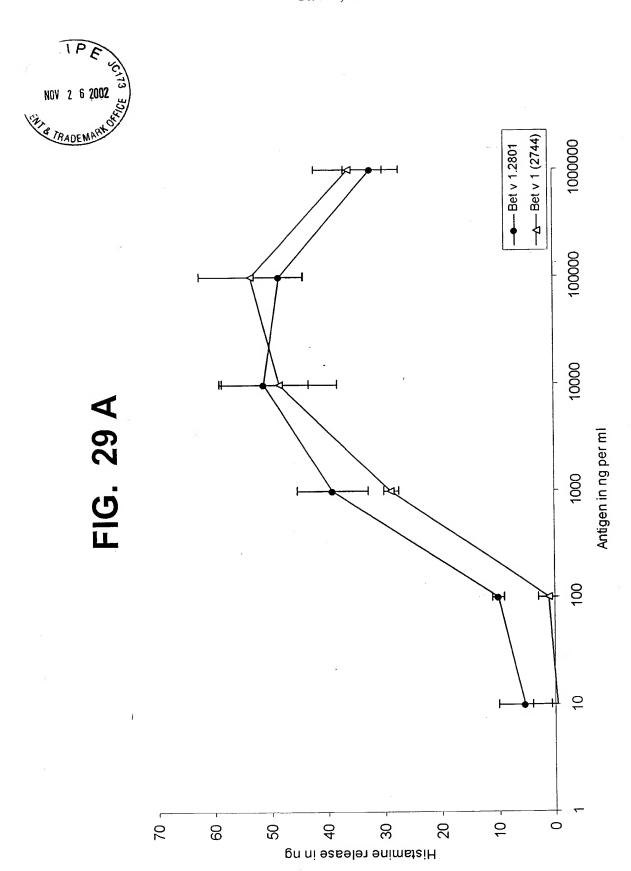


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Pristamine release in ng



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FIG. 29 B

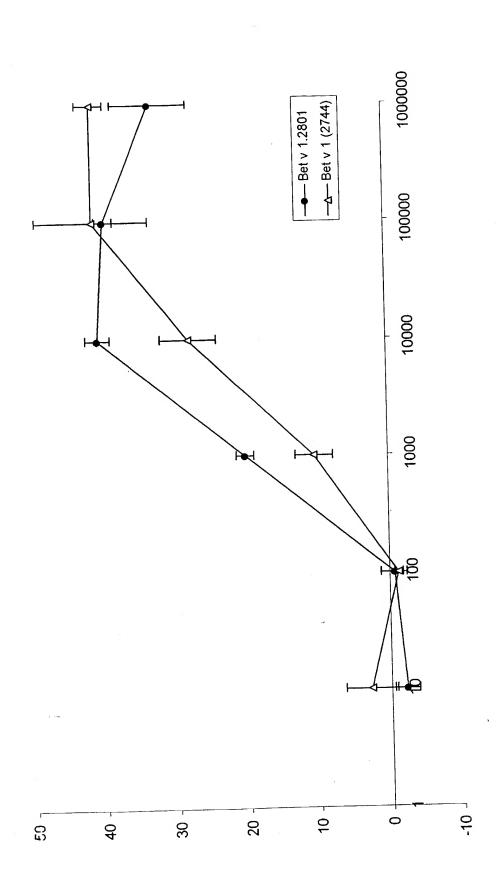
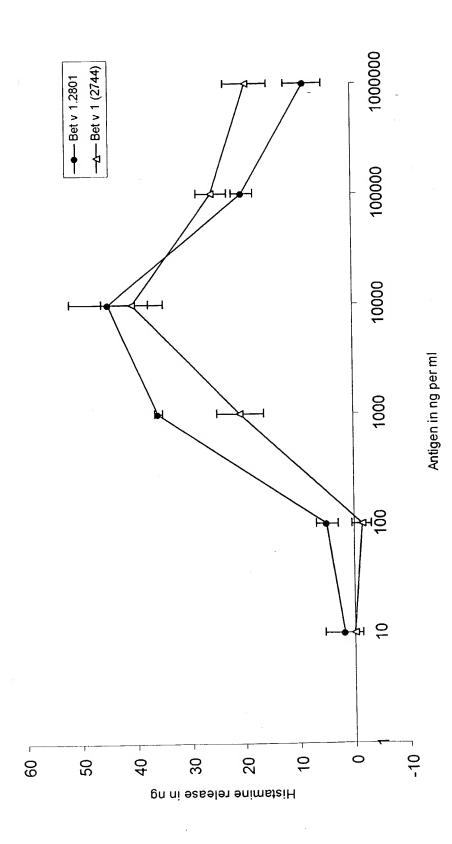




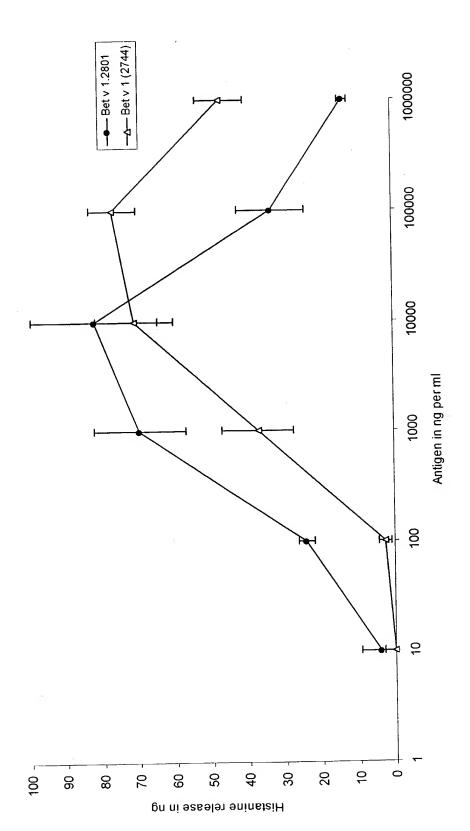
FIG. 29 C

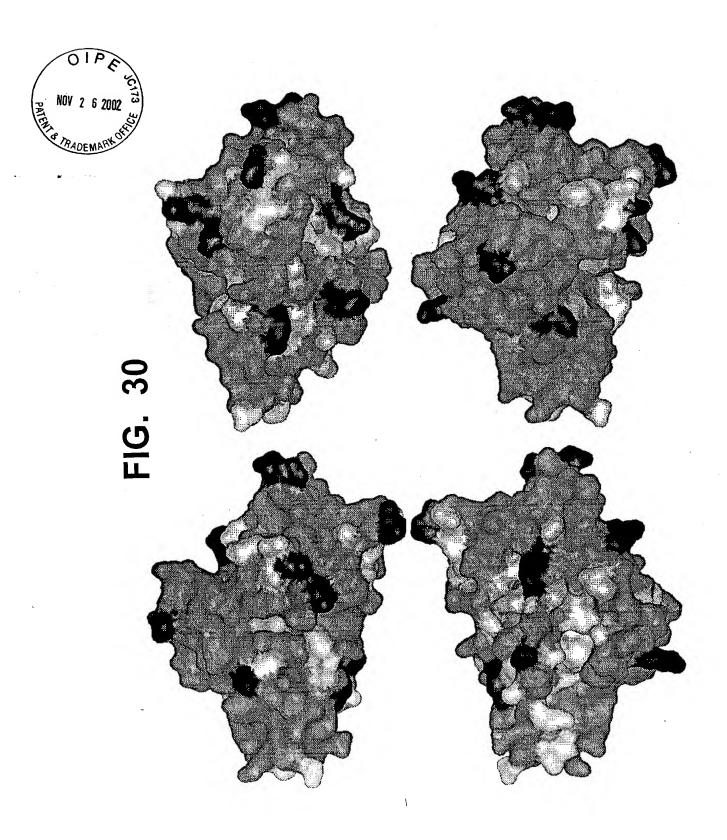


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FIG. 29 D







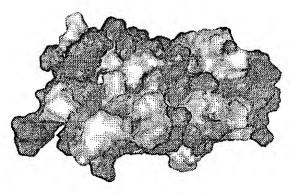
| K6A | sense | OB43 | 42-mer | 5' -CCG <u>CTCGAG</u> AAAAGAGATCAAGTCGATGTCGCCGATTGTGCC-3' | |
|------|------------|------|--------|---|--|
| | anti-sense | OB28 | 39-mer | Xba I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC- 3' | |
| K15E | sense | OB44 | 67-mer | Xho I 5' -CCG <u>CTCGAG</u> AAAAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTTGG- 3' | |
| | anti-sense | OB28 | 39-mer | Xba I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC- 3' | |
| H30N | sense | OB46 | 54-mer | Kpn I 5' -CGG <u>GGTACC</u> AGGATGTCATGGTTCAGAACCATGTATCATTAA CCGTGGTAAACC-3' | |
| | anti-sense | OB28 | 39-mer | Xba I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3' | |
| E62S | sense | OB47 | 33-mer | 5' -GCCTCAATCGATGGTTTATCAGTTGATGTTCCC-3' | |
| | anti-sense | OB48 | 33-mer | 5' -GGGAACATCAACTGATAAACCATCGATTGAGGC- 3' | |
| H74N | sense | OB49 | 32-mer | 5' -CATG <u>GCATGC</u> AATTACATGAAATGCCCATTGG- 3' | |
| | anti-sense | OB28 | 39-mer | Xba I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC- 3' | |
| K82N | sense | OB50 | 50-mer | Sph I 5'-CTACGCATGCCATTACATGAAATGCCCATTGGTTAATGGACAA (1970) (1970) (1970) (1970) (1970) | |
| | anti-sense | OB28 | 39-mer | Xba I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC- 3' | |

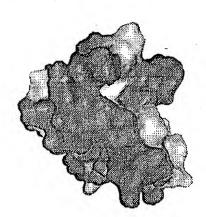
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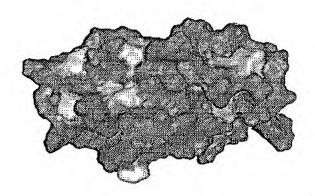
| 1 DERP2-ALK-G Der p 2 2 DERP 2 CONA Der p 2 3 DERP2-ISO101 Der p 2 4 DERP2-ISO102 Der p 2 5 DERP2-ISO103 Der p 2 6 DERP2-ISO103 Der p 2 7 DERP2-ISO103 Der p 2 7 DERP2-ISO103 Der p 2 8 1 ASV 9 DEF 2 DERFA Der f 2 9 DEF 2 DERFA Der f 2 | Der f 2 B61241 Der f 2 PDB Der f 2 A61501 Eur m 2 0107 096430 Eur m 2 0107 097722 | Der p 2 | 44XH- | 1 DERPZ-ALKG Der p 2 V K G Q D Q 2 DER P 2 CDNA Der p 2 V K G Q D Q Q D DER P 2 CDNA Der p 2 V K G Q D Q Q D DER P 2 CDNA Der p 2 V K G Q Q Q D D D D D D D D D D D D D D D D |
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| | 00000 00000 00000 00000 000000 | 2222222 2444444 244444444444444444444 | CEEEEE 1444777 100000 1444774 100000 | |



FIG. 33







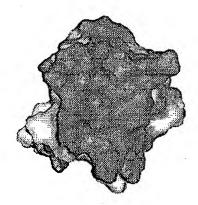




FIG. 34

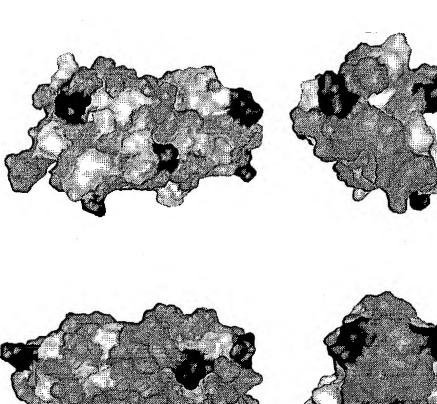




FIG. 35 A

| | Jer p1 ALK Jer p 1 Sur m 1.0101 | m 1.0101 m 1.0102 | Z E S | | 21 A K | 1 0 | iur m 1.0101 | m 1.0102 | Ţ | 11 11 | * * 1 | Ser p1 ALK Ser p 1 | m 1.0101 | Eur m 1.0102 Der f 1 | E 5 | |
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FIG. 35 B

| ************************************** | Der pl ALK P P P P P P P P P P P P P P P P P P | | Der pl ALK S A Eurm 1,0101 T A Eurm 1,0101 T A Eurm 1,0101 T A Eurm 1,0102 T A | | 大 3 数 数 3 000 | 9999 **\$\$ |
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| 0 8 | 7 | 1 4 0 | | 2 0 0 | 0 N G Y G Y F D N G Y G Y F D N G Y G Y F | 0 N G Y G Y F A 0 N G Y G Y F A 0 S G Y G Y F O 0 N G Y G Y F A |
| 0 6 | 00000000000000000000000000000000000000 | 150 | 0000000 D X X X X X O D X Y X X X X O D X Y X X X X X X X X X X X X X X X X X | 2 1 0 | A N I D L M A N I D L M A N I N I M | E E E . |
| - | 4444444 >>>>>>>> >>>>>> | - | | 2 | M E E Y P Y M E E Y P Y M E O Y P Y | |
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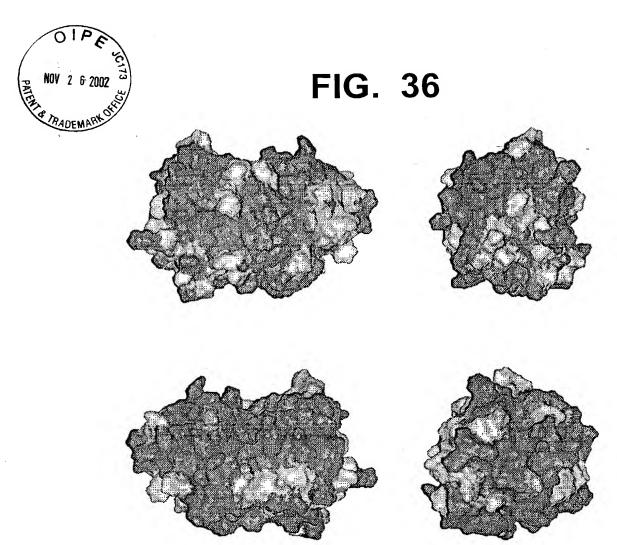
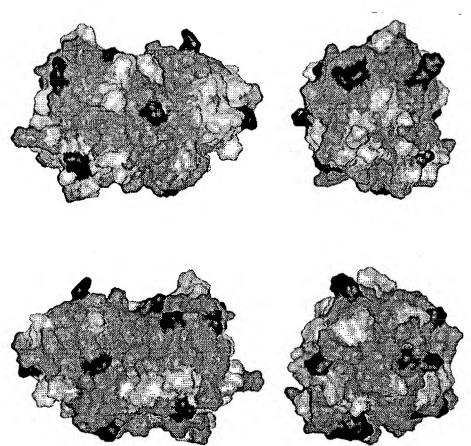




FIG. 37



| 1 | SIPE | 4 0000 | 1,24 | 5 |
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| | - municipal e | TRADEMANAS TIG. | . 38 A |
|--|-----------------------------|--|--|
| tr 081341 081341 | Phl p 5.0103 | | |
| trjQ40960[Q40960 | Phlp5 Phlp5A | MAVHQYTVALFLAVALV | |
| spiP22285 MP92_POAPR | Pos p 5 (KBG41) | | |
| sp P22286 MP93_POAPR tr O65319 O65319 | Phi p 5 (KBGou) | | |
| 1rj065320 065320 1rj065321 065321 | Phip5 Phip5 | | |
| trj065318 065318 | Phlp5 | | |
| triP93467 iP93467 spiP22284 iMP91_POAPR | Phl p 5 Poa o 5 (KBG 31) | | VFQATFDKNLK |
| splQ40237JMP5B_LOLPR | Lol p 5B | M A V Q K H T V A L F L A V A L V | |
| tr Q9XF24 Q9XF24 tr Q9SC99 Q9SC99 | Lol p 5A Lol p 5C | MAVQKYTVALFLAVALV | |
| trj081343 061343 | Phl p 5.0206 Hol I 5 | MAVQKYTVALFLAVALV | |
| trj023972 023972 trj081344 081344 | Phl p 5.0207 | MAVOKYTVALFLAVALV | |
| tn AAG42255 AAG42255 tn AAG42254 AAG42254 | Hol 15B Poa p 5 | MAVOKYTVALFLTVALV | |
| 11/081342/081342 | Phl p 5.0203 | S V K R S N G S A E V H R G A V P R R G P R | |
| tr/P93466 P93466 sp Q40963 MP5B_PHLPR | Phl p 5 Phl p 58 | AAAAVPRRGPR | |
| tr Q9SBE0 Q9SBE0 tr Q23971 Q23971 | Phi p 5.0204 Phi p 5.02 | | |
| | Pha a 5.3 | M A V Q K Y T V A L F L A M A L V | |
| HAAQ tri004828 004828 | Pha a 5.1 Hor v 9 | M A N S G R E H S A V P R R R N L V A | |
| tr Q39995 Q39995 | Hor v 5 (30kDa) | | |
| | | | |
| *************************************** | | 10 20 | 3 0 |
| tr 081341 081341 | PN p 5.0103 | ATPAAPAAGYTEATPAAPAG | AAPAGKAT. |
| triQ40960 Q40960 spiQ40962 MP5A_PHLPR | Phip 5 Phin 5 A | ATPAAPAAGYTPATPAAPAG | A D A A G N A T . |
| 8plP22285[MP92_POAPR | Pos p 5 (KBG41) | PATLATPATPAAPAGYIPAAPAU | |
| sp[P22286]MP93_POAPR tri0653191065319 | Posp 5 (KBG6U) Phip 5 | P | AAPAGKAT. |
| tr O65320 O65320 | Phlp5 | | A A P A G K A T . |
| tr 065321 065321 tr 065318 065318 | Phip5 Phip5 | GPATPAAPAE | A A P A G K A T . |
| 1/19934671993467 | Phip 5 Poap 5 (KBG 31) | PPASKEPAKPAPKVAAYIPAAPAG | A A P K A T . |
| splQ40237IMP5B_LOLPR | Lol p 5B | . ATPATPAAPATAAN PATPATPA | A A V P S G K A T . . т Р A A A G G K A T . |
| tr Q9XF24 Q9XF24 tr Q9SC99 Q9SC99 | Lol p 5A Lol p 5C | Y T P A A A A T P A T P A A | . TPAAGGGKAT . |
| tr 081343 081343 | Phl p 5.0206 | THE STATE OF THE ANGLE AND A STATE AND A S | A E . A G K A T . |
| tr 023972 023972 tr 081344 081344 | Hol 15 Phi p 5.0207 | Alpaterania G | AE . AG NAT : |
| tnjAAG42255jAAG42255 tnjAAG42254jAAG42254 | Hol 15B Poa p 5 | YAPATPAA AG | AA. AGKITP |
| 14081342 061342 | PM p 5.0203 | | AE AGKAT. |
| tr P93466 P93466 ep Q40963 MP58_PHLPR | Phip 5 Phip 58 | | AA. AGKAT. |
| triQ9SBE0jQ9SBE0 | Phl p 5.0204 | A A BUAR LEVA A BAG A BAG A BAG A BAG A BAG A | AE IAGKAI |
| tr/023971/023971 sp/P56166/MP53_PHAAQ | Phi p 5.02 Pha a 5.3 | A CONTRACTOR OF A CONTRACTOR O | . V P G A A A G K A T . . L P P P R A R D K A . |
| HAAQ | Pha a 5.1 Hor v 9 | | |
| tr 004828 004828 tr 039995 039995 | Hor v 5 (30kDa) | | |
| | | | |
| | | 90 100 1100 | 1 2 0 |
| tr O81341 O81341 | Phl p 5.0103 | EPKG - AAESSSKAALTSKLDAAYKLA | Y KI A E G A I P E A K Y KI A E G A II P E A K |
| triQ40960jQ40960 spiQ40962jMP5A_PHLPR | Phip5 Phip5A | EPRG. AAESSSKAALTSKLDAAYKLA FPRG. AAESSSKAALTSKLDAAYKLA | YKTAEGATPEAK |
| spiP22286 MP92_POAPR | Poa p 5 (KBG41) | EPKG A A A A S S NIA VILT S K L D A A Y K L A | Y K S A E G A T P E A K Y K S A E G A T P E A K |
| spiP22286jMP93_POAPR triQ65319jQ65319 | Posp 5 (KBG60) Phip 5 | EPKG. AAESSSKAALTSKLDAAYNLA | YKTAEGATPEAK |
| tr 065320 065320 | Phlp5 | EPKGAAFSSSKAALTSKLOAAYKLA | Y K T A E G A T P E A K Y K T A E G A T P E A K |
| tr O65321 O65321 tr O65318 O65318 | Phlp5 Phlp5 | EPKG. AAESSSKAALTSKLDAAYKLA | Y K T A E G A T P E A E Y K T S E G A T P E A K |
| triP93467 P93467 spiP22284 MP91_POAPR | Phi p 5 | EPKGAAESSSKGALTSALEAAYKLA EPKGAAVASSKAVLTSKUDAAYKLA | Y K T S E G A I P E A K Y K S A E G A T P E A K |
| spiQ40237IMP5B_LOLPR | Loi p 5B | G Y A D . Q S K N Q L T S K L D A A L K L A | Y E A A Q G A T P F A K Y K A A F G A T P F A K |
| 14Q9XF24 Q9XF24 14Q9SC99 Q9SC99 | Lot p 5A Lot p 5C | DAKAP GLILKLDTDYDVA | YKAGEGATPEAK |
| tr 081343 081343 | :Phl p 5.0206 | G L V P K L D A A Y S V A | Y K A A V G A T P E A K Y A A A Q G A T P E A K |
| trj023972 023972 trj081344 081344 | Hol I 5 PN p 5 0207 | GLVPKLBAAYSVS | YKAAVGATPEAK |
| tn AAG42255 AAG42255 | Hol I 5B | | YKAAVGATPEAK |
| tn AAG42254 AAG42254 1r OB1342 OB1342 | Poa p 5 Phl p 5 0203 | GUVPKLDAAYSVA | YKAAVGATPEAK |
| trjP93466jP93466 spjQ40963jMP5B_PHLPF | Phlp5 Phlp5B | AP. GLVPKLDAAYSVA | YKAAVGÄTPEAK |
| I/JQ9SBE0JQ9SBE0 | Phl p 5.0204 | AP GLVPKLDAAYSVA | Y K A A V G A T P E A K F K A S T G G T O E A K |
| tri023971 023971 apiP56166 MP53_PHAAG | Phi p 5.02 Phe a 5.3 | L DEARYSVV | YNTAAGATPEAK |
| HAAO | Pha a 5.1 | | Y D K A Q G A I P L A A |
| tr 004828 004828 tr Q39995 Q39995 | Hor v 9 Hor v 5 (30kDa) | A A 1 S U 1 A S U 3 A S A S A S A S A S A S A S A S A S A | YDKAOGATPEAK |

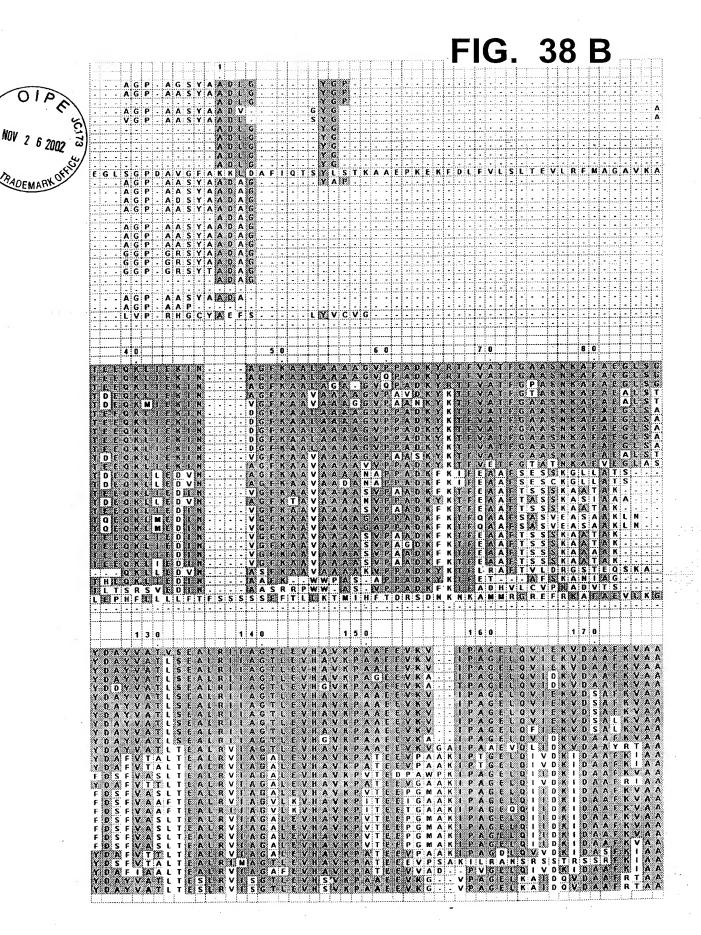




FIG. 38 C

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| AAQ | Pha a 5.1 | | <u>į</u> . | : : | | | | | . 23 | ΑĄ | HI S | | | | | | ۲. | | A. | | | A | Mi. | E L | | |
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| Q40990(040990) [040995]MP92_PhLPR [IP22265]MP92_POAPR [IP22265]MP93_POAPR 056319(06532) 06532(106532) 06532(106532) 06532(106532) 06532(1065316) P53467[P53467 [P22264]MP91_POAPR [IP22264]MP91_POAPR [IP22266]MP91_POAPR [IP22226]MP91_POAPR [IP22226]MP91_POAPR [IP22226]MP91_POAPR [IP222266]MP91_POAPR [IP22226]MP91_POAPR [IP222226]MP91_POAPR [IP222226]MP91_POAPR [IP22226]MP91_POAPR [IP22 | PNI p 5.0103 PNI p 5.0103 PNI p 5.0203 | 200 - 100 - | A A A A A A A A A A A A A A A A A A A | A | A | | | A | A A A A | | AAAAGAAAAGAGAAAAAAAAAAAAAAAAAAAAAAAAAA | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | 7 7 6 6 6 6 5 6 6 5 P > 2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | V V V V V V V V V A I T T T T T T T T T T T T T T T T T T | | | | P | | | · · · · · · · · · · · · · · · · · · · | | AAAAAAAAAAAA | | | A |
| G40980IQ40980 IGA40985IJMP52_PhLPR IJP22286JMP92_POAPR IJP22286JMP93_POAPR O65319IQ65319 O653210065320 O65321066321 O6532106521 O653210652 | PN p 5.0103 PN p 5.0103 PN p 5. PN p 5.0203 | | A A A A A A A A A A A A A A A A A A A | A | 4 | T \ | | A | A A A A | | AAAAGAAAAGAGGVGVAAVV | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | 7 7 0 G S S S S P V V X A A A A A A A A A A A A A A A A A | V V V V V V V V V A I T T T T T T T T T T T T T T T T T T | | | | P | | | · · · · · · · · · · · · · · · · · · · | | AAAAAAAAAAAAAAAA | | | A |
| [G40980]G40980 (G40980]MP92_POLPR IJP22286]MP92_POLPR IJP22286]MP93_POLPR IJP22286]MP93_POLPR IJP22286]MP93_POLPR IJP22386]MP93_POLPR IJP22386]MP93_POLPR IJP22386]MP93_POLPR IJP22386]MP95_POLPR IJP22386]MP95_POLPR IJP22386]MP95_POLPR IJP22386 IJP2386 IJP2386 IJP22386 IJ | Phi p 5.0103 Phi p 5.0 Phi p 5 A Poa p 5 (KBG60) Phi p 5 Phi p 5.0207 Phi p 5.0203 Phi p 5.0203 Phi p 5 Phi p 5.0204 | | A A A A A A A A C T C C C T C C C T C C C T C | A | A | T | , A | A (| A A A A | | AAAAGAAAAGAGGVGVAAVVX | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | 7 | V V V V V V V V V A I T T T T T T T T T T T T T T T T T T | | | | P | | A A A A A A A A A A A A A A A A A A A | T · · · · · · · · · · · · · · · · · · · | | AAAAATAAAAAAAAAAAA | | | A / |
| [G40960]G40960 [G40962]MP5A_PHLPR IJP22266[MP93_POAPR IJP22266[MP93_POAPR IJP22266[MP93_POAPR IJP22266[MP93_POAPR IJP22266[MP93_POAPR IJP2226[MP93]FP3467 IJP2226[MP99]FP347 IJP2226[MP99]FP347 IJP2226[MP99]FP347 IJP2226[MP99]FP347 IJP2226[MP99]FP347 | PN p 5.0103 PN p 5.0103 PN p 5.0103 PN p 5.0203 PN p 5.0203 PN p 5.0203 PN p 5.0204 | | A A A A A A A A A A A A A A A A A A A | A | A | · · · · · · · · · · · · · · · · · · · | , A | A (| A A A A | | A A A A A A A A A A A A A A A A A A A | A A A A A A A A A A A A A A A A A A A | 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | V 1 2 3 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | A | | | P | | A A A A A A A A A A A A A A A A A A A | · · · · · · · · · · · · · · · · · · · | | AAAAATAAAAAAAAAAAAAAAAA | | , A | A |
| pip22265 MP92 POAPR PP22266 MP93 POAPR O55319 O55319 O65320 O65320 O65320 O65321 O65320 O65321 O65319 O65318 P93467 P93467 P93467 P93467 P93467 P93467 D922261 MP91 POAPR D922261 MP91 POAPR D92227 MP91 POAPR D92227 MP91 POAPR D9227 MP91 POAPR D9327 MP91 POAPR D9327 MP91 POAPR D9327 MP91 POAPR D93461 D93971 PS6165 MP93 PHAAQ | PN p 5.0103 PN p 5.0103 PN p 5.A PN p 5.A PN p 5.A PN p 5.COG PN p 5. PN p 5.COG PN p 5.COGG PN p | | A A A A A A A A A A A A A A A A A A A | A | A | | , A | A (| - A A A A A A A A A A | | AAAAGAAAAGAGGUGUAAAAAAA | A A A A A A A A A A A A A A A A A A A | G S S S S S S S S S S S S S S S S S S S | VVVVVVVVATTTTTTTTTTTTTTTTTTTTTTTTTTTTT | | | A 1 | P | | A A A A A A A A A A A A A A A A A A A | · | | AAAAATAAAAAAAAAAAAAAAAA | S . | | A |
| [G40980]G40980 [G40982]MP92_POLPR pp22286]MP92_POLPR pp22286]MP93_POLPR pp22286]MP93_POLPR G6539[06533] G6532[106532] G6532[106532] G6532[106532] G6532[106532] G6532[106532] G65318[065318] P33467[P33467] P23467[P33467] P03467[P3467] G98729[03529] G9872[023972] | PN p 5.0103 PN p 5.0103 PN p 5.0103 PN p 5.0203 PN p 5.0203 PN p 5.0203 PN p 5.0204 | | A A A A A A A A A A A A A A A A A A A | A CONTRACTOR AND A CONT | PPP | | , A | A (| - A A A A A A A A A A | AAAVAAAAVAAAAAA - P | AAAAGAAAAGAGGUGUAAAAAAA | A A A A A A A A A A A A A A A A A A A | 7 0 A A A A A A A A A A A A A A A A A A | V V V V V V V V V A T T T T T T T T T T | | | A 1 | P | | A A A A A A A A A A A A A A A A A A A | · | | AAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | S . | A | A |



FIG. 38 D

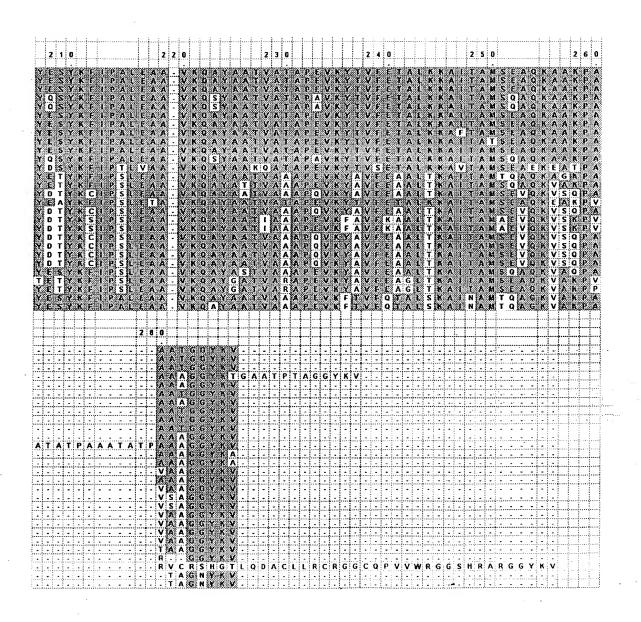
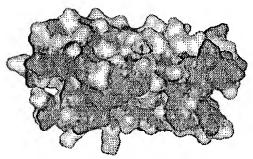
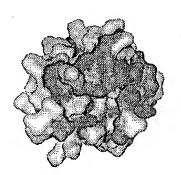
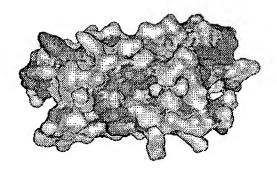




FIG. 39 A







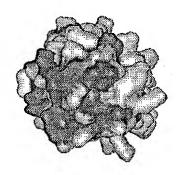
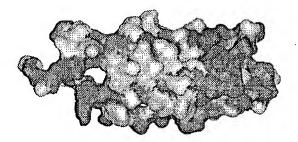
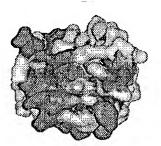
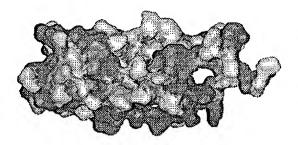




FIG. 39 B







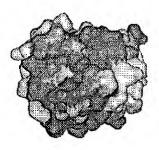
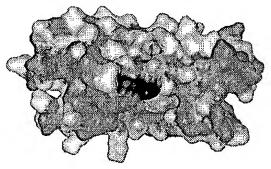
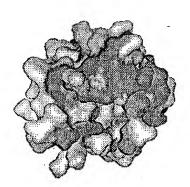
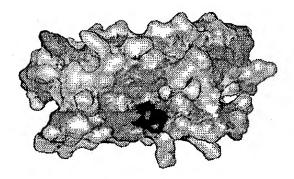




FIG. 40 A







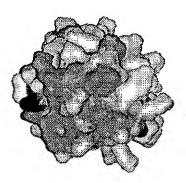
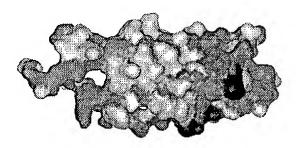
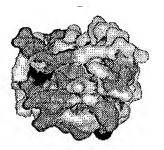
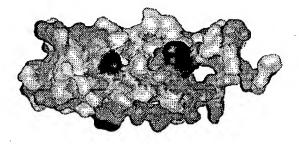


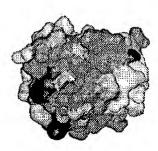


FIG. 40 B

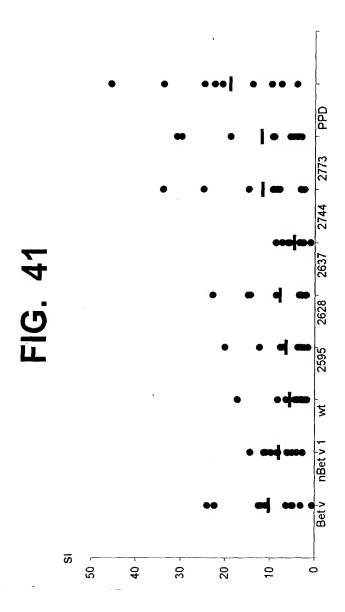






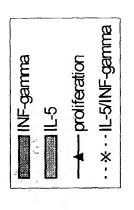






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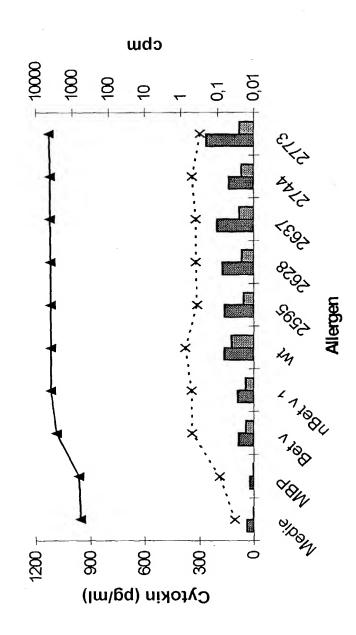
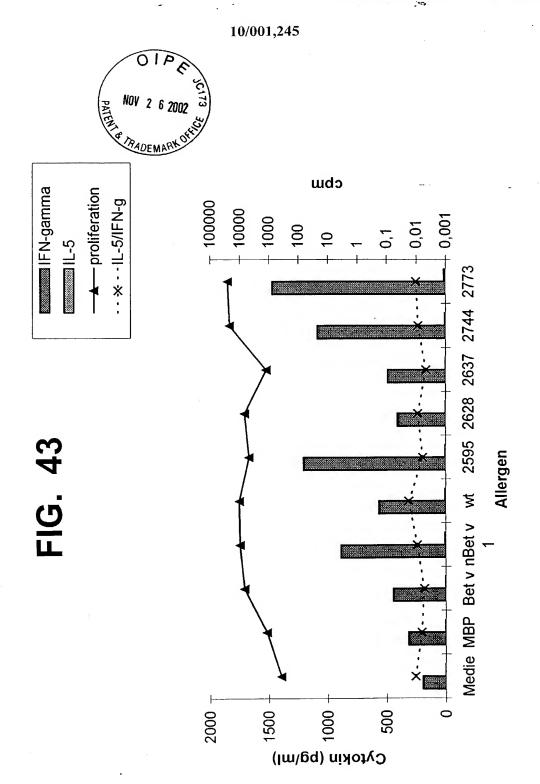
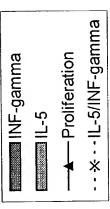


FIG. 42



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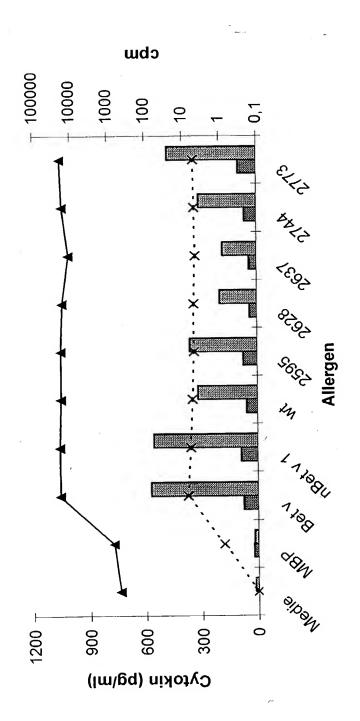


FIG. 44